



103

SEQUENCE LISTING

#6/a
chh
10-28-98

(1) GENERAL INFORMATION:

(i) APPLICANT:

Ullrich, Axel
Aoki, Naohito
Kim, Yeong Woong
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Naylor, Oliver
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(ii) TITLE OF INVENTION:

NOVEL PTP20, PCP-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS

(iii) NUMBER OF SEQUENCES:

35

(iv) CORRESPONDENCE ADDRESS:

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Suite 4700
(C) CITY: Los Angeles
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/877,150
(B) FILING DATE: JUNE 17, 1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: U.S. 60/019,629
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(B) FILING DATE: November 13, 1996

(A) APPLICATION NUMBER: U.S. 60/030,964
(B) FILING DATE: November 15, 1996

(A) APPLICATION NUMBER: U.S. 60/034,286
(B) FILING DATE: December 19, 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 225/298

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(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 3 and 5 stands
for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Trp Xaa Met Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 6 stands for
either Ser, Ile or Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His Cys Ser Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Phe Leu Glu Arg Leu Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 3 and 5 stands
for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Arg Trp Xaa Met Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 6 stands for
either Ser, Ile or Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

His Cys Ser Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTCTGTGTCC ACAGCAGTGC TGGCTGT

27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

His Arg Asp Leu Ala Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for
Val or Met. "Xaa" in position
5 stands for Tyr or Phe.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Xaa Trp Ser Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGGGATCCCT TCGCCTTGCA GCTTTGTC

28

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGAATTCCT AGACTGATAC AGTCTGTAAG

30

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Leu Lys Pro Glu Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Met Met Glu Arg Ile
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATAGCGGCC GCTAGACTGA TACAGTCTGT

30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCCCCCGGGA TGCCCCATCC CCGAAGGTAC CA

32

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATAGCGGCC GCTCACCGAC TGATATCCCG ACTGGAGTC

39

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCCCCCGGGG AGACGATGCA TCACTGTAAG

30

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TATAGCGGCC GCGCTGGCCT GCACCTGTCA TCTGCTGGG

39

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CGGAATTCAT GCGGCATTCC AAACGAACTC

30

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TATAGCGGCC GCCCTGACTC CCACTCATTT CCTTTTAA

39

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGAATTCCG CCACCATGGC CCCTATACTA GGTTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCCAAGCTTG CCACCATGGC CCCTATACTA GGTTAT

36

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTAGCAGTAA GAATAGTTAA A

21

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTTGCCCTGA GGATCATTA GAAT

24

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTGCCCTGA GGATCATCCG GAAT

24

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TACAATTCTC ACTGCTACAT GTAAGCCATC

30

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Pro Ile Tyr Ser Phe Ile Gly Gly Glu His Phe Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ile Val Glu Pro Asp Thr Glu Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Tyr Gly Phe Ser Pro Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Ile Lys Glu Val Ala His Val Asn Leu Glu Val Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Ala Ala Gly Asp Ser Ala Thr
 1 5

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 28...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GAATTCCGGC ACGAGGCGGG TTGCAGT ATG AGT CGC CAA TCG GAC CTA GTG AGG	54
Met Ser Arg Gln Ser Asp Leu Val Arg	
1 5	
AGC TTC TTG GAG CAG CAG GAG GCC CGG GAC CAC CGG AAG GGG GCA ATC	102
Ser Phe Leu Glu Gln Gln Glu Ala Arg Asp His Arg Lys Gly Ala Ile	
10 15 20 25	
CTC GCC CGT GAG TTC AGC GAC ATT AAG GCC CGC TCA GTG GCT TGG AAG	150
Leu Ala Arg Glu Phe Ser Asp Ile Lys Ala Arg Ser Val Ala Trp Lys	
30 35 40	
ACT GAA GGT GTG TGC TCC ACT AAA GCC GGC AGT CAG CAG GGA AAC TCA	198
Thr Glu Gly Val Cys Ser Thr Lys Ala Gly Ser Gln Gln Gly Asn Ser	
45 50 55	
AAG AAG AAC CGC TAC AAA GAC GTG GTA CCG TAT GAT GAG ACG AGA GTC	246
Lys Lys Asn Arg Tyr Lys Asp Val Val Pro Tyr Asp Glu Thr Arg Val	
60 65 70	
ATC CTT TCC CTG CTC CAG GAG GAA GGA CAC GGA GAT TAC ATT AAT GCC	294
Ile Leu Ser Leu Leu Gln Glu Gly His Gly Asp Tyr Ile Asn Ala	
75 80 85	
AAC TTC ATC CGG GGC ACA GAT GGA AGC CAG GCC TAC ATT GCG ACG CAA	342
Asn Phe Ile Arg Gly Thr Asp Gly Ser Gln Ala Tyr Ile Ala Thr Gln	
90 95 100 105	
GGA CCC CTG CCT CAC ACT CTG TTG GAC TTC TGG CGC CTG GTT TGG GAG	390
Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp Arg Leu Val Trp Glu	
110 115 120	
TTT GGA ATC AAG GTG ATC TTG ATG GCC TGT CAG GAG ACA GAA AAT GGA	438
Phe Gly Ile Lys Val Ile Leu Met Ala Cys Gln Glu Thr Glu Asn Gly	
125 130 135	
CGG AGG AAG TGT GAA CGC TAC TGG GCC CAG GAG CGG GAG CCT CTA CAG	486
Arg Arg Lys Cys Glu Arg Tyr Trp Ala Gln Glu Arg Glu Pro Leu Gln	
140 145 150	
GCC GGG CCT TTC TGC ATC ACC CTG ACA AAG GAG ACA GCA CTG ACT TCG	534
Ala Gly Pro Phe Cys Ile Thr Leu Thr Lys Glu Thr Ala Leu Thr Ser	
155 160 165	
GAC ATC ACT CTC AGG ACC CTC CAG GTT ACA TTC CAG AAG GAA TCC CGT	582
Asp Ile Thr Leu Arg Thr Leu Gln Val Thr Phe Gln Lys Glu Ser Arg	
170 175 180 185	
CCT GTG CAC CAG CTA CAG TAC ATG TCT TGG CCG GAC CAC GGG GTT CCC	630
Pro Val His Gln Leu Gln Tyr Met Ser Trp Pro Asp His Gly Val Pro	
190 195 200	

AGC	AGT	TCC	GAT	CAC	ATT	CTC	ACC	ATG	GTG	GAG	GAG	GCC	CGT	TGC	CTC	678
Ser	Ser	Ser	Asp	His	Ile	Leu	Thr	Met	Val	Glu	Glu	Ala	Arg	Cys	Leu	
			205					210					215			
CAA	GGA	CTT	GGA	CCT	GGA	CCC	CTC	TGT	GTC	CAC	TGC	AGT	GCT	GGC	TGT	726
Gln	Gly	Leu	Gly	Pro	Gly	Pro	Leu	Cys	Val	His	Cys	Ser	Ala	Gly	Cys	
		220					225					230				
GGA	CGA	ACA	GGT	GTC	TTG	TGT	GCT	GTT	GAT	TAC	GTG	AGG	CAG	TTG	CTT	774
Gly	Arg	Thr	Gly	Val	Leu	Cys	Ala	Val	Asp	Tyr	Val	Arg	Gln	Leu	Leu	
	235					240					245					
CTG	ACT	CAG	ACA	ATC	CCA	CCC	AAT	TTC	AGC	CTC	TTT	GAA	GTG	GTC	CTG	822
Leu	Thr	Gln	Thr	Ile	Pro	Pro	Asn	Phe	Ser	Leu	Phe	Glu	Val	Val	Leu	
	250				255					260					265	
GAG	ATG	CGG	AAA	CAG	CGA	CCT	GCA	GCG	GTG	CAG	ACA	GAG	GAG	CAG	TAC	870
Glu	Met	Arg	Lys	Gln	Arg	Pro	Ala	Ala	Val	Gln	Thr	Glu	Glu	Gln	Tyr	
				270					275					280		
AGG	TTC	CTG	TAC	CAC	ACA	GTG	GCT	CAG	CTA	TTC	TCC	CGC	ACT	CTC	CAG	918
Arg	Phe	Leu	Tyr	His	Thr	Val	Ala	Gln	Leu	Phe	Ser	Arg	Thr	Leu	Gln	
			285					290					295			
AAC	AAC	AGT	CCC	CTC	TAC	CAG	AAC	CTC	AAG	GAG	AAC	CGC	GCT	CCA	ATC	966
Asn	Asn	Ser	Pro	Leu	Tyr	Gln	Asn	Leu	Lys	Glu	Asn	Arg	Ala	Pro	Ile	
		300					305					310				
TGC	AAG	GAC	TCC	TCG	TCC	CTC	AGG	ACC	TCC	TCA	GCC	CTG	CCT	GCC	ACA	1014
Cys	Lys	Asp	Ser	Ser	Ser	Leu	Arg	Thr	Ser	Ser	Ala	Leu	Pro	Ala	Thr	
	315					320					325					
TCC	CGC	CCA	CTG	GGT	GGC	GTT	CTC	AGG	AGC	ATC	TCG	GTG	CCT	GGG	CCA	1062
Ser	Arg	Pro	Leu	Gly	Gly	Val	Leu	Arg	Ser	Ile	Ser	Val	Pro	Gly	Pro	
	330				335					340					345	
CCG	ACC	CTT	CCC	ATG	GCT	GAC	ACT	TAC	GCT	GTG	GTG	CAG	AAG	CGT	GGC	1110
Pro	Thr	Leu	Pro	Met	Ala	Asp	Thr	Tyr	Ala	Val	Val	Gln	Lys	Arg	Gly	
				350					355					360		
GCT	TCC	GGC	AGC	ACA	GGG	CCG	GGC	ACG	CGG	GCG	CCC	AAC	AGC	ACG	GAC	1158
Ala	Ser	Gly	Ser	Thr	Gly	Pro	Gly	Thr	Arg	Ala	Pro	Asn	Ser	Thr	Asp	
			365					370					375			
ACC	CCG	ATC	TAC	AGC	CAG	GTG	GCT	CCA	CGT	ATC	CAG	CGG	CCC	GTG	TCA	1206
Thr	Pro	Ile	Tyr	Ser	Gln	Val	Ala	Pro	Arg	Ile	Gln	Arg	Pro	Val	Ser	
		380					385					390				
CAC	ACC	GAA	AAC	GCG	CAG	GGG	ACA	ACG	GCA	CTG	GGC	CGA	GTT	CCT	GCG	1254
His	Thr	Glu	Asn	Ala	Gln	Gly	Thr	Thr	Ala	Leu	Gly	Arg	Val	Pro	Ala	
		395				400					405					
GAT	GAA	AAC	CCT	TCC	GGG	CCT	GAT	GCC	TAT	GAG	GAA	GTA	ACA	GAT	GGA	1302
Asp	Glu	Asn	Pro	Ser	Gly	Pro	Asp	Ala	Tyr	Glu	Glu	Val	Thr	Asp	Gly	
	410				415					420				425		
GCG	CAG	ACT	GGT	GGG	CTA	GGC	TTC	AAC	TTG	CGC	ATT	GGA	AGA	CCT	AAA	1350
Ala	Gln	Thr	Gly	Gly	Leu	Gly	Phe	Asn	Leu	Arg	Ile	Gly	Arg	Pro	Lys	
				430					435					440		

GGG CCA CGG GAT CCT CCA GCG GAG TGG ACA CGG GTG TAATGAGTGC TGTACC 1402
 Gly Pro Arg Asp Pro Pro Ala Glu Trp Thr Arg Val
 445 450

AGTTCCAGCC TGTCACCTCAG TGGTGGCTGG GCGACTGCAA CCCCCATGCT GCTGTGTGCT 1462
 GTCTTATGTA TGAGTGGGAC TCATGGGCCT GAATCAAAAT AAAAGTTTCT CAGGGGTAGAA 1522
 AAAAAACAAAT AGGGACTTTG GCCAGTGGTT ATAGCAGTCA AAGCCAGGGG CTAGGAGGGG 1582
 TAAGTGGGGG AGGTGGTGGA TCTACTCTGA GAAAGTTTAG GAAAGCACAT CAAGAGTGAG 1642
 CATCGCCACT CTTCTCCCCA TACACCTACT GGAAAGTGCA CCCCAGACAG AGTCCTAACT 1702
 TGACAGTGCA CCTCAGACAG GTCGCTACCT GGATGGACAT GCTGGCCCTA CAGCTAGAGA 1762
 CATGTCTAAT TAGATCCTCA TGTAAACTTG CAATGAGCTA GAAAGATCTC CGTCTGGTCA 1822
 GGGAAATGGA TCACCTAGTC AGGTAAATAG TGTGCCATCC AGAAGACAGA ACTGCAAGAT 1882
 ACCGTCTTTT TCAAAATGGA AGAAAATAGA TCCTCAAGAA TAAATGTATG TACAATGCTC 1942
 TACGCCCTGA TCCTGCCCTG CCTCACTGCC ATAATGTCAC AAACAAGTCA GGGTCTATAT 2002
 GACAGTTGTT CATCTAGTCA GTCCTGACTG TGGCCTCTGC AGGCTCAGAT AGTGCCTTCT 2062
 GCAGACTCTT GGAATGCCCG TCTTGAACCT GATGAAAGCT TCTACCGGGA ACTTGTAAC 2122
 ATCATTAATA TTATTAATGT AGAATTCAAT AAAGAGTGGG TCAAAAACCTC AAAAAAAAAA 2182
 AAAAAAAAAA AAAAAAACTC GAGAGTACTT CTAGAGCGGG CGGG 2226

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 133...4422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTCCGGGC GCCAGTCCCG CTCCGCGCCG CGCCGCTCCG CTCCGGCTCG GGCTCCGGCT 60
 CGCCTCGGGC TGGGCTCGGG CTCCGGGGGC GGCGTCCCCG CGCCGGGCCC CGGGACGCGC 120
 CGACCTCCAA CC ATG GCC CGT GCC CAG GCG CTC GTG CTG GCA CTC ACC TTC 171
 Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe
 1 5 10
 CAG CTC TGC GCG CCG GAG ACC GAG ACT CCG GCA GCT GGC TGC ACC TTC 219
 Gln Leu Cys Ala Pro Glu Thr Glu Thr Pro Ala Ala Gly Cys Thr Phe
 15 20 25
 GAG GAG GCA AGT GAC CCA GCA GTG CCC TGC GAG TAC AGC CAG GCC CAG 267
 Glu Glu Ala Ser Asp Pro Ala Val Pro Cys Glu Tyr Ser Gln Ala Gln
 30 35 40 45
 TAC GAT GAC TTC CAG TGG GAG CAA GTG CGA ATC CAC CCT GGC ACC CGG 315
 Tyr Asp Asp Phe Gln Trp Glu Gln Val Arg Ile His Pro Gly Thr Arg
 50 55 60
 GCA CCT GCG GAC CTG CCC CAC GGC TCC TAC TTG ATG GTC AAC ACT TCC 363
 Ala Pro Ala Asp Leu Pro His Gly Ser Tyr Leu Met Val Asn Thr Ser
 65 70 75
 CAG CAT GCC CCA GGC CAG CGA GCC CAT GTC ATC TTC CAG AGC CTG AGC 411
 Gln His Ala Pro Gly Gln Arg Ala His Val Ile Phe Gln Ser Leu Ser
 80 85 90

GAG Glu	AAT Asn	GAT Asp	ACC Thr	CAC His	TGT Cys	GTG Val	CAG Gln	TTC Phe	AGC Ser	TAC Tyr	TTC Phe	CTG Leu	TAC Tyr	AGC Ser	CGG Arg	459
95						100					105					
GAC Asp	GGC Gly	ACA Thr	GGC Gly	GGC Gly	ACC Thr	CTG Leu	CGC Arg	GTC Val	TAC Tyr	GTG Val	CGC Arg	GTT Val	AAT Asn	GGG Gly	GGC Gly	507
110					115					120					125	
CCC Pro	CTG Leu	GCG Ala	AGT Ser	GCT Ala	GTG Val	TGG Trp	AAT Asn	ATG Met	ACT Thr	GGA Gly	TCC Ser	CAC His	GGC Gly	CGT Arg	CAG Gln	555
				130					135					140		
TGG Trp	CAC His	CAG Gln	GCT Ala	GAG Glu	CTG Leu	GCT Ala	GTC Val	AGC Ser	ACT Thr	TTC Phe	TGG Trp	CCC Pro	AAT Asn	GAA Glu	TAT Tyr	603
			145					150					155			
CAG Gln	GTG Val	CTG Leu	TTT Phe	GAG Glu	GCC Ala	CTC Leu	ATC Ile	TCC Ser	CCA Pro	GAC Asp	CGC Arg	AGG Arg	GGC Gly	TAC Tyr	ATG Met	651
		160					165					170				
GGC Gly	CTA Leu	GAT Asp	GAC Asp	ATC Ile	CTG Leu	CTT Leu	CTC Leu	AGC Ser	TAC Tyr	CCC Pro	TGC Cys	GCA Ala	AAG Lys	GCC Ala	CCA Pro	699
175						180					185					
CAC His	TTC Phe	TCC Ser	CGC Arg	CTG Leu	GGC Gly	GAC Asp	GTG Val	GAG Glu	GTC Val	AAC Asn	GCG Ala	GGC Gly	CAG Gln	AAC Asn	GCG Ala	747
190					195					200					205	
TCG Ser	TTC Phe	CAG Gln	TGC Cys	ATG Met	GCC Ala	GCG Ala	GGA Gly	GAG Glu	CCC Pro	ATG Met	CGC Arg	CAA Gln	CGC Arg	TTC Phe	CTC Leu	795
				210					215					220		
TTG Leu	CAA Gln	CGG Arg	CAG Gln	AGC Ser	GGG Gly	GCC Ala	CTG Leu	GTG Val	CCG Pro	GCC Ala	GGG Gly	GCG Ala	TTC Phe	GGC Gly	ACA Thr	843
			225					230					235			
TCA Ser	GCC Ala	ACC Thr	GGC Gly	TTC Phe	CTG Leu	GCC Ala	ACT Thr	TTC Phe	CCG Pro	CTG Leu	GCT Ala	GCC Ala	GTG Val	AGC Ser	CGC Arg	891
		240					245					250				
GCC Ala	GAG Glu	CAG Gln	GAC Asp	CTG Leu	TAC Tyr	CGC Arg	TGT Cys	GTG Val	TCC Ser	CAG Gln	GCC Ala	CCG Pro	CGC Arg	GGC Gly	GGC Gly	939
255						260					265					
GTC Val	TCT Ser	AAC Asn	TTC Phe	CCG Pro	GAG Glu	CTC Leu	ATC Ile	GTC Val	AAG Lys	GAG Glu	CCC Pro	CCA Pro	ACT Thr	CCC Pro	ATC Ile	987
270					275					280					285	
GCG Ala	CCC Pro	CCA Pro	CAG Gln	CTG Leu	CTG Leu	CGT Arg	GCT Ala	GGC Gly	CCC Pro	ACC Thr	TAC Tyr	CTC Leu	ATC Ile	ATC Ile	CAG Gln	1035
				290					295					300		
CTC Leu	AAC Asn	ACC Thr	AAC Asn	TCC Ser	ATC Ile	ATT Ile	GGC Gly	GAC Asp	GGG Gly	CCG Pro	ATC Ile	GTG Val	CGC Arg	AAG Lys	GAG Glu	1083
			305					310					315			
ATT Ile	GAG Glu	TAC Tyr	CGC Arg	ATG Met	GCG Ala	CGC Arg	GGG Gly	CCC Pro	TGG Trp	GCT Ala	GAG Glu	GTG Val	CAC His	GCC Ala	GTC Val	1131
		320					325					330				

AGC Ser	CTG Leu	CAG Gln	ACC Thr	TAC Tyr	AAG Lys	CTG Leu	TGG Trp	CAC His	CTC Leu	GAC Asp	CCC Pro	GAC Asp	ACA Thr	GAC Asp	TAT Tyr	1179
	335					340					345					
GAG Glu	ATC Ile	AGC Ser	GTG Val	CTG Leu	CTC Leu	ACG Thr	CGT Arg	CCC Pro	GGA Gly	GAC Asp	GGC Gly	GGC Gly	ACT Thr	GGC Gly	CGC Arg	1227
	350				355					360					365	
TGG Trp	GCC Ala	ACC Thr	CCT Pro	CAT His	CAG Gln	CCG Pro	CAC His	CAA Gln	ATG Met	CGC Arg	AGA Arg	GCC Ala	CAT His	GAG Glu	GGC Gly	1275
				370					375					380		
CCC Pro	AAA Lys	GGC Gly	CTG Leu	GCT Ala	TTT Phe	GCT Ala	GAG Glu	ATC Ile	CAG Gln	GCC Ala	CGT Arg	CAG Gln	CTG Leu	ACC Thr	CTG Leu	1323
			385					390					395			
CAG Gln	TGG Trp	GAA Glu	CCA Pro	CTG Leu	GGC Gly	TAC Tyr	AAC Asn	GTG Val	ACG Thr	CGT Arg	TGC Cys	CAC His	ACC Thr	TAT Tyr	ACT Thr	1371
	400						405					410				
GTG Val	TCG Ser	CTG Leu	TGC Cys	TAT Tyr	CAC His	TAC Tyr	ACC Thr	CTG Leu	GGC Gly	AGC Ser	AGC Ser	CAC His	AAC Asn	CAG Gln	ACC Thr	1419
	415					420					425					
ATC Ile	CGA Arg	GAG Glu	TGT Cys	GTG Val	AAG Lys	ACA Thr	GAG Glu	CAA Gln	GGT Gly	GTC Val	AGC Ser	CGC Arg	TAC Tyr	ACC Thr	ATC Ile	1467
	430				435					440					445	
AAG Lys	AAC Asn	CTG Leu	CTG Leu	CCC Pro	TAT Tyr	CGG Arg	AAC Asn	GTT Val	CAC His	GTG Val	AGG Arg	CTT Leu	GTC Val	CTC Leu	ACT Thr	1515
				450					455					460		
AAC Asn	CCT Pro	GAG Glu	GGG Gly	CGC Arg	AAA Lys	GAG Glu	GGC Gly	AAG Lys	GAG Glu	GTC Val	ACT Thr	TTC Phe	CAG Gln	ACG Thr	GAT Asp	1563
			465					470					475			
GAG Glu	GAT Asp	GTG Val	CCC Pro	AGT Ser	GGG Gly	ATT Ile	GCA Ala	GCC Ala	GAG Glu	TCC Ser	CTG Leu	ACC Thr	TTC Phe	ACT Thr	CCA Pro	1611
	480						485					490				
CTG Leu	GAG Glu	GAC Asp	ATG Met	ATC Ile	TTC Phe	CTC Leu	AAG Lys	TGG Trp	GAG Glu	GAG Glu	CCC Pro	CAG Gln	GAG Glu	CCC Pro	AAT Asn	1659
	495					500					505					
GGT Gly	CTC Leu	ATC Ile	ACC Thr	CAG Gln	TAT Tyr	GAG Glu	ATC Ile	AGC Ser	TAC Tyr	CAG Gln	AGC Ser	ATC Ile	GAG Glu	TCA Ser	TCA Ser	1707
	510				515				520					525		
GAC Asp	CCG Pro	GCA Ala	GTG Val	AAC Asn	GTG Val	CCA Pro	GGC Gly	CCA Pro	CGA Arg	CGT Arg	ACC Thr	ATC Ile	TCC Ser	AAG Lys	CTC Leu	1755
				530					535					540		
CGC Arg	AAT Asn	GAG Glu	ACC Thr	TAC Tyr	CAT His	GTC Val	TTC Phe	TCC Ser	AAC Asn	CTG Leu	CAC His	CCA Pro	GGC Gly	ACC Thr	ACC Thr	1803
			545					550					555			
TAC Tyr	CTG Leu	TTC Phe	TCC Ser	GTG Val	CGG Arg	GCC Ala	CGC Arg	ACA Thr	GGC Gly	AAA Lys	GGC Gly	TTC Phe	GGC Gly	CAG Gln	GCG Ala	1851
		560					565					570				

GCA	CTC	ACT	GAG	ATA	ACC	ACT	AAC	ATC	TCT	GCT	CCC	AGC	TTT	GAT	TAT	1899
Ala	Leu	Thr	Glu	Ile	Thr	Thr	Asn	Ile	Ser	Ala	Pro	Ser	Phe	Asp	Tyr	
	575					580					585					
GCC	GAC	ATG	CCG	TCA	CCC	CTG	GGC	GAG	TCT	GAG	AAC	ACC	ATC	ACC	GTG	1947
Ala	Asp	Met	Pro	Ser	Pro	Leu	Gly	Glu	Ser	Glu	Asn	Thr	Ile	Thr	Val	
590					595					600					605	
CTG	CTG	AGG	CCG	GCA	CAG	GGC	CGC	GGT	GCG	CCC	ATC	AGT	GTG	TAC	CAG	1995
Leu	Leu	Arg	Pro	Ala	Gln	Gly	Arg	Gly	Ala	Pro	Ile	Ser	Val	Tyr	Gln	
				610					615					620		
GTG	ATT	GTG	GAG	GAG	GAG	CGG	GCG	CGA	GGC	TGC	GGC	GGG	ACG	AGG	TGG	2043
Val	Ile	Val	Glu	Glu	Glu	Arg	Ala	Arg	Gly	Cys	Gly	Gly	Thr	Arg	Trp	
			625					630					635			
ACA	GGA	CTG	CTT	CCC	AGT	GCC	ATT	GAC	CTT	CGA	GGC	GGC	GCT	GGC	CCC	2091
Thr	Gly	Leu	Leu	Pro	Ser	Ala	Ile	Asp	Leu	Arg	Gly	Gly	Ala	Gly	Pro	
		640					645					650				
AGG	CTG	GTG	CAC	TAC	TTC	GGG	GCC	GAA	CTG	GCG	GCC	AGC	AGT	CTA	CCT	2139
Arg	Leu	Val	His	Tyr	Phe	Gly	Ala	Glu	Leu	Ala	Ala	Ser	Ser	Leu	Pro	
	655					660					665					
GAG	GCC	ATG	CCC	TTT	ACC	GTG	GGT	GAC	AAC	CAG	ACC	TAC	CGA	GGC	TTC	2187
Glu	Ala	Met	Pro	Phe	Thr	Val	Gly	Asp	Asn	Gln	Thr	Tyr	Arg	Gly	Phe	
670					675					680					685	
TGG	AAC	CCA	CCA	CTT	GAG	CCT	AGG	AAG	GCC	TAT	CTC	ATC	TAC	TTC	CAG	2235
Trp	Asn	Pro	Pro	Leu	Glu	Pro	Arg	Lys	Ala	Tyr	Leu	Ile	Tyr	Phe	Gln	
				690					695					700		
GCA	GCA	AGC	CAC	CTG	AAG	GGG	GAG	ACC	CGG	CTG	AAT	TGC	ATC	CGC	ATT	2283
Ala	Ala	Ser	His	Leu	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Cys	Ile	Arg	Ile	
			705					710					715			
GCC	AGG	AAA	GCT	GCC	TGC	AAG	GAA	AGC	AAG	CGG	CCC	CTG	GAG	GTG	TCC	2331
Ala	Arg	Lys	Ala	Ala	Cys	Lys	Glu	Ser	Lys	Arg	Pro	Leu	Glu	Val	Ser	
		720					725					730				
CAG	AGA	TCG	GAG	GAG	ATG	GGG	CTT	ATC	CTG	GGC	ATC	TGT	GCA	GGG	GGG	2379
Gln	Arg	Ser	Glu	Glu	Met	Gly	Leu	Ile	Leu	Gly	Ile	Cys	Ala	Gly	Gly	
	735					740					745					
CTT	GCT	GTC	CTC	ATC	CTT	CTC	CTG	GGT	GCC	ATC	ATT	GTC	ATC	ATC	CGC	2427
Leu	Ala	Val	Leu	Ile	Leu	Leu	Leu	Gly	Ala	Ile	Ile	Val	Ile	Ile	Arg	
750					755					760					765	
AAA	GGG	AAG	CCG	GTG	AAC	ATG	ACC	AAG	GCC	ACC	GTC	AAC	TAC	CGC	CAG	2475
Lys	Gly	Lys	Pro	Val	Asn	Met	Thr	Lys	Ala	Thr	Val	Asn	Tyr	Arg	Gln	
				770					775					780		
GAG	AAG	ACA	CAC	ATG	ATC	AGC	GCC	GTG	GAC	CGC	AGC	TTC	ACA	GAC	CAG	2523
Glu	Lys	Thr	His	Met	Ile	Ser	Ala	Val	Asp	Arg	Ser	Phe	Thr	Asp	Gln	
			785					790					795			
AGC	ACC	CTG	CAG	GAG	GAC	GAG	CGG	CTG	GGC	CTG	TCC	TTC	ATG	GAC	ACC	2571
Ser	Thr	Leu	Gln	Glu	Asp	Glu	Arg	Leu	Gly	Leu	Ser	Phe	Met	Asp	Thr	
		800					805					810				

CAT His 815	GGC Gly	TAC Tyr	AGC Ser	ACC Thr	CGG Arg	GGA Gly 820	GAC Asp	CAG Gln	CGC Arg	AGC Ser	GGT Gly 825	GGG Gly	GTC Val	ACT Thr	GAG Glu	2619
GCC Ala 830	AGC Ser	AGC Ser	CTC Leu	CTG Leu	GGG Gly 835	GGC Gly	TCC Ser	CCG Pro	AGG Arg	CGT Arg 840	CCC Pro	TGT Cys	GGC Gly	CGG Arg	AAG Lys 845	2667
GGC Gly	TCC Ser	CCA Pro	TAC Tyr	CAC His 850	ACG Thr	GGG Gly	CAG Gln	CTG Leu	CAC His 855	CCT Pro	GCG Ala	GTG Val	CGT Arg	GTC Val 860	GCA Ala	2715
GAC Asp	CTT Leu	CTG Leu	CAG Gln 865	CAC His	ATC Ile	AAC Asn	CAG Gln	ATG Met 870	AAG Lys	ACG Thr	GCC Ala	GAG Glu	GGT Gly 875	TAC Tyr	GGC Gly	2763
TTC Phe	AAG Lys	CAG Gln 880	GAG Glu	TAT Tyr	GAG Glu	AGC Ser	TTC Phe 885	TTT Phe	GAA Glu	GGC Gly	TGG Trp	GAC Asp 890	GCC Ala	ACA Thr	AAG Lys	2811
AAG Lys 895	AAA Lys	GAC Asp	AAG Lys	GTC Val	AAG Lys	GGC Gly 900	AGC Ser	CGG Arg	CAG Gln	GAG Glu	CCA Pro 905	ATG Met	CCT Pro	GCC Ala	TAT Tyr	2859
GAT Asp 910	CGG Arg	CAC His	CGA Arg	GTG Val	AAA Lys 915	CTG Leu	CAC His	CCG Pro	ATG Met	CTG Leu 920	GGA Gly	GAC Asp	CCC Pro	AAT Asn	GCC Ala 925	2907
GAC Asp	TAC Tyr	ATT Ile	AAT Asn	GCC Ala 930	AAC Asn	TAC Tyr	ATA Ile	GAT Asp	GGT Gly 935	TAC Tyr	CAC His	AGG Arg	TCA Ser	AAC Asn 940	CAC His	2955
TTC Phe	ATA Ile	GCC Ala	ACT Thr 945	CAA Gln	GGG Gly	CCG Pro	AAG Lys	CCT Pro 950	GAG Glu	ATG Met	GTC Val	TAT Tyr	GAC Asp 955	TTC Phe	TGG Trp	3003
CGT Arg	ATG Met	GTG Val 960	TGG Trp	CAG Gln	GAG Glu	CAC His	TGT Cys 965	TCC Ser	AGC Ser	ATC Ile	GTC Val	ATG Met 970	ATC Ile	ACC Thr	AAG Lys	3051
CTG Leu 975	GTC Val	GAG Glu	GTG Val	GGC Gly	AGG Arg	GTG Val 980	AAA Lys	TGC Cys	TCA Ser	CGG Arg	TAC Tyr 985	TGG Trp	CCG Pro	GAG Glu	GAC Asp	3099
TCA Ser 990	GAC Asp	ACC Thr	TAC Tyr	GGG Gly	GAC Asp 995	ATC Ile	AAG Lys	ATT Ile	ATG Met 1000	CTG Leu	GTG Val	AAG Lys	ACA Thr	GAG Glu 1005	ACC Thr	3147
CTG Leu	GCT Ala	GAG Glu	TAT Tyr	GTC Val 1010	GTG Val	CGC Arg	ACT Thr	TTT Phe	GCC Ala 1015	CTG Leu	GAG Glu	CGG Arg	AGA Arg	GGC Gly 1020	TAC Tyr	3195
TCT Ser	GCC Ala	CGG Arg	CAC His 1025	GAG Glu	GTC Val	CGC Arg	CAG Gln	TCC Ser 1030	CAC His	TTC Phe	ACA Thr	GCG Ala 1035	TGG Trp	CCA Pro	GAG Glu	3243
CAT His	GGC Gly	GTC Val 1040	CCC Pro	TAC Tyr	CAT His	GCC Ala 1045	ACG Thr	GGG Gly	CTG Leu	CTG Leu	GCT Ala 1050	TTC Phe	ATC Ile	CGG Arg	CGG Arg	3291

GTG AAG GCC TCC ACC CCA CCT GAT GCC GGG CCC ATT GTC ATC CAC TGC	3339
Val Lys Ala Ser Thr Pro Pro Asp Ala Gly Pro Ile Val Ile His Cys	
1055 1060 1065	
AGC GCG GGC ACC GGC CGC ACA CGT TGC TAT ATC GTC CTG GAT GTG ATG	3387
Ser Ala Gly Thr Gly Arg Thr Arg Cys Tyr Ile Val Leu Asp Val Met	
1070 1075 1080 1085	
CTG GAC ATG GCA GAG TGT GAG GGC GTC GTG GAC ATT TAC AAC TGT GTG	3435
Leu Asp Met Ala Glu Cys Glu Gly Val Val Asp Ile Tyr Asn Cys Val	
1090 1095 1100	
AAG ACT CTC TGC TCC CGG CGT GTC AAC ATG ATC CAG ACT GAG GAG CAG	3483
Lys Thr Leu Cys Ser Arg Arg Val Asn Met Ile Gln Thr Glu Glu Gln	
1105 1110 1115	
TAC ATC TTC ATT CAT GAT GCA ATC CTG GAG GCC TGC CTG TGT GGG GAG	3531
Tyr Ile Phe Ile His Asp Ala Ile Leu Glu Ala Cys Leu Cys Gly Glu	
1120 1125 1130	
ACC ACC ATC CCT GTC AGT GAG TTC AAG GCC ACC TAC AAG GAG ATG ATC	3579
Thr Thr Ile Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu Met Ile	
1135 1140 1145	
CGC ATT GAT CCT CAG AGT AAT TCC TCC CAG CTG CGG GAA GAG TTC CAG	3627
Arg Ile Asp Pro Gln Ser Asn Ser Ser Gln Leu Arg Glu Glu Phe Gln	
1150 1155 1160 1165	
ACG CTG AAC TCG GTC ACC CCG CCG CTG GAC GTG GAG GAG TGC AGC ATC	3675
Thr Leu Asn Ser Val Thr Pro Pro Leu Asp Val Glu Glu Cys Ser Ile	
1170 1175 1180	
GCC CTG TTG CCC CGG AAC CGC GAC AAG AAC CGC AGC ATG GAC GTC CTG	3723
Ala Leu Leu Pro Arg Asn Arg Asp Lys Asn Arg Ser Met Asp Val Leu	
1185 1190 1195	
CCG CCC GAC CGC TGC CTG CCC TTC CTC ATC TCC ACT GAT GGG GAC TCC	3771
Pro Pro Asp Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly Asp Ser	
1200 1205 1210	
AAC AAC TAC ATT AAT GCA GCC CTG ACT GAC AGC TAC ACA CGG AGG TCG	3819
Asn Asn Tyr Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg Arg Ser	
1215 1220 1225	
GCC TTC ATG GTG ACC CTG CAC CCG CTG CAG AGC ACC ACG CCC GAC TTC	3867
Ala Phe Met Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe	
1230 1235 1240 1245	
TGG CGG CTG GTC TAC GAT TAC GGG TGC ACC TCC ATC GTC ATG CTC AAC	3915
Trp Arg Leu Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn	
1250 1255 1260	
CAG CTG AAC CAG TCC AAC TCC GCC TGG CCC TGC CTG CAG TAC TGG CCA	3963
Gln Leu Asn Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro	
1265 1270 1275	
GAG CCA GGC CGG CAG CAA TAT GGC CTC ATG GAG GTG GAG TTT ATG TCG	4011
Glu Pro Gly Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser	
1280 1285 1290	

GGC ACA GCT GAT GAA GAC TTA GTG GCT CGA GTC TTC CGG GTG CAG AAC Gly Thr Ala Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn 1295 1300 1305	4059
ATC TCT CGG TTG CAG GAG GGA GAC CTG CTG GTG CGG CAC TTC CAG TTC Ile Ser Arg Leu Gln Gly Asp Leu Leu Val Arg His Phe Gln Phe 1310 1315 1320 1325	4107
CTG CGC TGG TCT GCA TAC CGG GAC ACA CCT GAC TCC AAG AAG GCC TTC Leu Arg Trp Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe 1330 1335 1340	4155
TTG CAC CTG CTG GCT GAG GTG GAC AAG TGG CAG GCC GAG AGT GGG GAT Leu His Leu Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp 1345 1350 1355	4203
GGG CGC ACC ATC GTG CAC TGC CTA AAC GGG GGA GGA CGC AGC GGC ACC Gly Arg Thr Ile Val His Cys Leu Asn Gly Gly Arg Ser Gly Thr 1360 1365 1370	4251
TTC TGC GCC TGC GCC ACG GTC CTG GAG ATG ATC CGC TGC CAC AAC TTG Phe Cys Ala Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu 1375 1380 1385	4299
GTG GAC GTT TTC TTT GCT GCC CAA ACC CTC CGG AAC TAC AAA CCC AAC Val Asp Val Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn 1390 1395 1400 1405	4347
ATG GTG GAG ACC ATG GAT CAG TAC CAC TTT TGC TAC GAT GTG GCC CTG Met Val Glu Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu 1410 1415 1420	4395
GAG TAC TTG GAG GGG CTG GAG TCA AGA TAGCGGGGCC CTGGCCTGGG GCACCCA Glu Tyr Leu Glu Gly Leu Glu Ser Arg 1425 1430	4449
CTGCACACTC AGGGCCAGAC CCACCATCCT GGAAGATCAG TGCCTCCTGC TCTGCCCCAA CACACTCCCA TGGGGCAAGC ACTGGAGTGG ATGCTGGGCT ATCTTGCTCC CCCTTCCACT GTGGGCAGGG CCTTTCGCTT GTCCCATGGG CGGGTGGTGG GCCAAGGAGG AGCTTAGCAA GTCTGCACCC CACCCCAACC TCCATAGGGT CCTGCAGGCC TGTGCTGAGA GGCCTGGTGC TGCCTGGCAG AGTGACAAAG GCTCAGGACG GCTGGCTCTG GGGGACTCAG GCCAAGGGGG TTGGCAGGAT CCTGGGTTTT GGGAGGGATG AGTGAGGCCC TGCAGAGAGC ATCCCAGGCC AAGGTTCCCA CTCAGCCTGC CCCCTCTGCA TGTGGGTAGA GGATGTACTG GGACTTGGCA TTTAGGATTC CATCTGGGGG ACCCCCTGAA GGTCCCCCCC AAGCAGGTCT CAATTCTGAT AGCCAGTGGG GCACACTGAC TGTCTCTCCC AGGGGAAGT CAGCGCCCTC CTCCCCACTG CCCCCTCCAG CCCCTGAGAT ATTTTGCTCA CTATCCCTCC CCACTTGCTT CCCTGATATG TGCTCTGACT TCCCTGAACC AGGATCTGCC TATTACTGCT GTCCCATGGG GGGCTCCTTC CCTGCCTGAC CCACTGTTGC AGAATGAAGT CACCTCGCCC CCCTCTTCCT TTAATCTTCA GGCCTCACTG GCCTGTCTTG CTCAGCTTGG GCCAGTGACA ATCTGCAAGG CTGAACAACA GCCCCTGGGG TTGAGGCCCC TGTGGCTCCT GGTCAGGCTG CCCGTTGTGG GGAGGGGCAG TGTTAGAGCA GGGCTGGTCA TACCTCTGG AGTTCAGAGC AAGAGGTAGG ACCAAGTCTT TTTTGTCTT TTTGTATTT TTGGTTGGGT GGGTGGGAAG GTCTCTTTAA AATGGGGCAG GCCACACCCC CATTCCTGTC CTCAATTTCC CCATCTGTAA ACTGTAGATA TGACTACTGA CCTACCTCGC AGGGGGCTGT GGGGAGGCAT AAGCTGATGT TTGTAAAGCG CTTTGTAAAT AAACGTGCTC TCTGAATGCC AAAAAAAAAA AAACAAAAAA AA	4509 4569 4629 4689 4749 4809 4869 4929 4989 5049 5109 5169 5229 5289 5349 5409 5469 5529 5581

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNES: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 44...1417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GAATTCGGCA CGAGCGGGCT GGACCTTGCT CGCCGCGGC GCC	ATG AGC CGC AGC	55
	Met Ser Arg Ser	
	1	
CTG GAC TCG GCG CCG AGC TTC CTG GAG CGG CTG GAA GCG CGG GGC GGC		103
Leu Asp Ser Ala Pro Ser Phe Leu Glu Arg Leu Glu Ala Arg Gly Gly		
5 10 15 20		
CGG GAG GGG GCA GTC CTC GCC GGC GAG TTC AGC GAC ATC CAG GCC TGC		151
Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp Ile Gln Ala Cys		
25 30 35		
TCG GCC GCC TGG AAG GCT GAC GGC GTG TGC TCC ACC GTG GCC GGC AGT		199
Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr Val Ala Gly Ser		
40 45 50		
CGG CCA GAG AAC GTG AGG AAG AAC CGC TAC AAA GAC GTG CTG CCT TAT		247
Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr		
55 60 65		
GAT CAG ACG CGA GTA ATC CTC TCC CTG CTC CAG GAA GAG GGA CAC AGC		295
Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu Glu Gly His Ser		
70 75 80		
GAC TAC ATT AAT GGC AAC TTC ATC CGG GGC GTG GAT GGA AGC CTG GCC		343
Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp Gly Ser Leu Ala		
85 90 95 100		
TAC ATT GCC ACG CAA GGA CCC TTG CCT CAC ACC CTG CTA GAC TTC TGG		391
Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp		
105 110 115		
AGA CTG GTC TGG GAG TTT GGG GTC AAG GTG ATC CTG ATG GCC TGT CGA		439
Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu Met Ala Cys Arg		
120 125 130		
GAG ATA GAG AAT GGG CGG AAA AGG TGT GAG CGG TAC TGG GCC CAG GAG		487
Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr Trp Ala Gln Glu		
135 140 145		
CAG GAG CCA CTG CAG ACT GGG CTT TTC TGC ATC ACT CTG ATA AAG GAG		535
Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr Leu Ile Lys Glu		
150 155 160		

AAG Lys 165	TGG Trp	CTG Leu	AAT Asn	GAG Glu	GAC Asp 170	ATC Ile	ATG Met	CTC Leu	AGG Arg	ACC Thr 175	CTC Leu	AAG Lys	GTC Val	ACA Thr	TTC Phe 180	583
CAG Gln	AAG Lys	GAG Glu	TCC Ser	CGT Arg 185	TCT Ser	GTG Val	TAC Tyr	CAG Gln 190	CTA Leu	CAG Gln	TAT Tyr	ATG Met	TCC Ser 195	TGG Trp	CCA Pro	631
GAC Asp	CGT Arg	GGG Gly	GTC Val 200	CCC Pro	AGC Ser	AGT Ser	CCT Pro	GAC Asp 205	CAC His	ATG Met	CTC Leu	GCC Ala 210	ATG Met	GTG Val	GAG Glu	679
GAA Glu	GCC Ala	CGT Arg 215	CGC Arg	CTC Leu	CAG Gln	GGA Gly 220	TCT Ser	GGC Gly	CCT Pro	GAA Glu	CCC Pro	CTC Leu 225	TGT Cys	GTC Val	CAC His	727
TGC Cys 230	AGT Ser	GCG Ala	GGT Gly	TGT Cys	GGG Gly 235	CGA Arg	ACA Thr	GGC Gly	GTC Val	CTG Leu 240	TGC Cys	ACC Thr	GTG Val	GAT Asp	TAT Tyr	775
GTG Val 245	AGG Arg	CAG Gln	CTG Leu	CTC Leu	CTG Leu 250	ACC Thr	CAG Gln	ATG Met	ATC Ile	CCA Pro 255	CCT Pro	GAC Asp	TTC Phe	AGT Ser	CTC Leu 260	823
TTT Phe	GAT Asp	GTG Val	GTC Val	CTT Leu 265	AAG Lys	ATG Met	AGG Arg	AAG Lys	CAG Gln 270	CGG Arg	CCT Pro	GCG Ala	GCC Ala	GTG Val 275	CAG Gln	871
ACA Thr	GAG Glu	GAG Glu 280	CAG Gln	TAC Tyr	AGG Arg	TTC Phe	CTG Leu	TAC Tyr 285	CAC His	ACG Thr	GTG Val	GCT Ala 290	CAG Gln	ATG Met	TTC Phe	919
TGC Cys	TCC Ser	ACA Thr 295	CTC Leu	CAG Gln	AAT Asn	GCC Ala 300	AGC Ser	CCC Pro	CAC His	TAC Tyr	CAG Gln	AAC Asn 305	ATC Ile	AAA Lys	GAG Glu	967
AAT Asn 310	TGT Cys	GCC Ala	CCA Pro	CTC Leu	TAC Tyr	GAC Asp 315	GAT Asp	GCC Ala	CTC Leu	TTC Phe	CTC Leu 320	CGG Arg	ACT Thr	CCC Pro	CAG Gln	1015
GCA Ala 325	CTT Leu	CTC Leu	GCC Ala	ATA Ile	CCC Pro 330	CGC Arg	CCA Pro	CCA Pro	GGA Gly	GGG Gly 335	GTC Val	CTC Leu	AGG Arg	AGC Ser	ATC Ile 340	1063
TCT Ser	GTG Val	CCC Pro	GGG Gly	TCC Ser 345	CCG Pro	GGC Gly	CAC His	GCC Ala	ATG Met 350	GCT Ala	GAC Asp	ACC Thr	TAC Tyr	GCG Ala 355	GAG Glu	1111
GAG Glu	CAG Gln	AAG Lys	CGC Arg 360	GGG Gly	GCT Ala	CCA Pro	GCG Ala	GGC Gly 365	GCC Ala	GGG Gly	AGT Ser	GGG Gly	ACG Thr 370	CAG Gln	ACG Thr	1159
GGG Gly	ACG Thr	GGG Gly 375	ACG Thr	GGG Gly	GCG Ala	CGC Arg	AGG Arg 380	GCG Ala	GAG Glu	GAG Glu	GCG Ala	CCG Pro 385	CTC Leu	TAC Tyr	AGC Ser	1207
AAG Lys 390	GTG Val	ACG Thr	CCG Pro	CGC Arg	GCC Ala	CAG Gln 395	CGA Arg	CCC Pro	GGG Gly	GCG Ala	CAC His 400	GCG Ala	GAG Glu	GAC Asp	GCG Ala	1255

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AGG GGG ACG CTG CCT GGC CGC GTT CCT GCT GAC CAA AGT CCT GCC GGA      1303
Arg Gly Thr Leu Pro Gly Arg Val Pro Ala Asp Gln Ser Pro Ala Gly
405                      410                      415                      420

TCT GGC GCC TAC GAG GAC GTG GCG GGT GGA GCT CAG ACC GGT GGG CTA      1351
Ser Gly Ala Tyr Glu Asp Val Ala Gly Gly Ala Gln Thr Gly Gly Leu
425                      430                      435

GGT TTC AAC CTG CGC ATT GGG AGG CCG AAG GGT CCC CGG GAC CCG CCT      1399
Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro
440                      445                      450

GCT GAG TGG ACC CGG GTG TAAGTCTAAC GCCAGTTCCT GCCTGTTGCC TCTTGTGA      1455
Ala Glu Trp Thr Arg Val
455

GCTCGGACTG CTGATGCCCC GGTGCTGCTG AGCGCCGTGC CGAGAATGGA AACAGTGGGC      1515
CTGGATCAAA GTTAAAGTTT CTCAGGGTGG GAAATGTGGG GGCTTTGCCC AATGACTGTA      1575
GCATTCAAGG CTTGAGGCTG GAGGAGGTAG CTAGGGTATA GTGGCTGGTG AGGCTGCACA      1635
GAGCAGATTC AAGAAAGAAG ATCAGGAAGG GGCATGACCC CTGAGTTATG AAGGGGAGAA      1695
GGGACAGATG AGCTTCCGGA GACTGCTCTC CTCACCACAC AGCACTAGTC CATCCTCAGC      1755
ACCTGAGCCT CCCTCACTTG GACACTCAGG GGACCACACA GAGAAGTGGA TGGACACTTC      1815
GCCATCCAGG CAGAACTAAG CCAGGCATAA CCACAGCCAA GCAGATTAAC CCCAGGCAGA      1875
CCGATAAAAA GACCTCCAGA TAGGCAGACA GACAGATGGA CCACCAACCT GGACAGACAG      1935
CCAAAGCTTC AGAGATACAG TCCACAGGTG GACAAAGGAT CCCCCAGCCA GAGAGAGAGA      1995
GACCAGCCAA CAGCTTGATA GACCAGTGCA GCCAGAGAGA CCACCAAACA CAGCCCCCAA      2055
AAGACAGACA TCTCTGCTAG CTGGACAGCC AGGTGGACCC CCTAAGTTAG TCAGATTACT      2115
AGACAGATAT AAACAGATCC CCTGCTGAAC AGATATACAG AGTTCTCAGA CCCCCTCCC      2175
TCAGGTGGGC TGGCTGGCTG ACAGACCTTC TGGCCAGACA GACTCCTAAC CAACCAGATG      2235
GACTGCCAGA CAGGCAGACA TCAGTCCACA TGGAATCCTG ACATCCCAGC CAGCCGGCCA      2295
GACTCTCATC TTGATGTCTT GATGGATGGA CCCCAGCTAG TCAGACATGA TCCTCCAGAT      2355
TGACAGACAA GTCCCCCAA TGAGTACACA TCTCCAGCTA TTCAGACAGA TGGAGCCCCA      2415
GCAAATCAGG ACCTATCTAG GCAGACCCCA GCCAGACCCC CGCCAGACAG ACTCCCAACC      2475
AGACTGACCC CTTGCTGTTT ACACAGCCTG CCGAGTAGCT GGGACTACAG GTCTAATTTT      2535
TTTTTTTTTT AAGAAATGAG TTTTGGCCAT GTTGCCGAGA CTGGTCTTGA ACTCCCAACC      2595
TCAAGCAATC CTCCTGCCTC AGCCTCCCAA AGTGTCTGAG TTACAGGTGT GAGCCACCAG      2655
GCTCAGCCCC CTAAGATTTG AAACACTTTA AATGGCCCAT GGTAGGGTTC CTGCTAGGAT      2715
AAAACATTAA GTGGCTGTTA AAAGAAATAA AAGGAGGACA CGTCTCTGTG CAAAAAAAAA      2775
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA
2810

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(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1              5              10              15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20              25              30

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Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly
 35 40 45
 Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
 50 55 60
 Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr
 65 70 75 80
 Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
 85 90 95
 Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
 100 105 110
 Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 115 120 125
 Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
 145 150 155 160
 Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175
 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
 260 265 270
 Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
 305 310 315 320
 Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
 340 345 350
 Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
 355 360 365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
 370 375 380
 Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
 385 390 395 400
 Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
 405 410 415
 Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
 420 425 430
 Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
 435 440 445
 His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
 450 455 460
 Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
 465 470 475 480
 Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
 485 490 495
 Ser Val Gln Val Pro Arg Lys
 500

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Pro Val Pro Ala Ser Trp Pro His Leu Pro Ser Pro Phe Leu Leu
 1 5 10 15
 Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu
 20 25 30
 Leu Gln Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly Glu
 35 40 45
 Ser Ala Thr Leu Arg Cys Ala Met Thr Ser Leu Ile Pro Val Gly Pro
 50 55 60
 Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn
 65 70 75 80
 Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Leu Thr
 85 90 95

Lys Arg Asn Asn Leu Asn Phe Ser Ile Ser Ile Ser Asn Ile Thr Pro
 100 105 110
 Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro
 115 120 125
 Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr
 145 150 155 160
 Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175
 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Ala Gly Asp Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Arg Val Val Leu Thr Arg Gly Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Met Ala His Ile Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Met Arg Ala Glu Asn Gln Ala Asn Val Thr Cys
 260 265 270
 Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Leu Thr Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Thr Cys
 305 310 315 320
 Ala His Arg Asp Asp Val Val Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln
 340 345 350
 Lys Glu His Gly Ser Asp Ile Thr His Glu Pro Ala Leu Ala Pro Thr
 355 360 365
 Ala Pro Leu Leu Val Ala Leu Leu Leu Gly Pro Lys Leu Leu Leu Val
 370 375 380
 Val Gly Val Ser Ala Ile Tyr Ile Cys Trp Lys Gln Lys Ala
 385 390 395